

Remarks

The application is to be amended as previously set forth to more closely conform the application to United States practice. All amendments are made without prejudice or disclaimer. Specifically, the claims are amended to clarify the claims and to remove multiple dependencies and to reduce the number of dependent claims.

Respectfully submitted,



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Enclosure: Version With Markings to Show Changes Made

APPENDIX A
VERSION WITH MARKINGS TO SHOW CHANGES MADE

21. (Amended) The purified and isolated polypeptide or fragment thereof, according to [claims 19 or 20] claim 19, wherein said amino acid sequence comprises at least 70% homology with SEQ ID NO: 1B, SEQ ID NO: 2B, or fragment of either thereof.

27. (Amended) A recombinant expression vector comprising:
a coding sequence operably linked to a promoter sequence and capable of directing expression of said coding sequence in a host cell of said vector, said coding sequence comprising [the] an isolated DNA sequence [according to any one of claims 1 to 18] encoding a polypeptide or fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology with SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit; and
a transcription termination sequence.

28. (Amended) A replicative cloning vector comprising:
the isolated DNA sequence of [any one of claims 1 to 18] encoding a polypeptide or fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO:

2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology with SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit; and
a replicon operative in a host cell for said vector.

29. (Amended) A method for regulating aliphatic and/or aromatic ester formation in fruit, comprising inserting one or more copies of one or more isolated DNA sequences - [according to claims 1 to 18] encoding a polypeptide or fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology with SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit into a genome of a fruit-producing plant.

31. (Amended) A plant and propagating material thereof comprising a genome including the vector according to [claims 27 or 28] claim 27.

32. (Amended) A genetically modified strawberry or lemon plant and propagating material derived therefrom, comprising a genome having an expression vector for over-expression or down-regulation of an endogenous strawberry or lemon plant gene counterpart of [the] an isolated DNA [sequences of claims 1 to 18] encoding a polypeptide or fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said

polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit.

33. (Amended) A method of producing aromatic and/or aliphatic esters in a microorganism, plant cell, or plant, comprising:
inserting one or more copies of [the] an isolated DNA [sequences of claims 1 to 18] encoding a polypeptide or fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit; and
feeding an alcohol CoA and an acyl-CoA to the microorganism, plant cell or plant.

36. (Amended) A method for regulating aliphatic and/or aromatic ester formation in fruit comprising inserting into the genome of a fruit-producing plant one or more copies of [one or more] the DNA [sequences as defined in any of claims 1-18] sequence encoding a polypeptide or

fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit.

37. (Amended) A genetically modified strawberry or lemon plant and propagating material derived therefrom which has a genome comprising an expression vector for overexpression or downregulation of an endogenous strawberry or lemon plant gene counterpart of [any of the] an isolated DNA [sequences as defined in claims 1 -18] encoding a polypeptide or fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit.

38. (Amended) A method for producing aromatic and/or aliphatic esters in a microorganism, plant cell or plant, comprising:
inserting into the genome of the microorganism or plant one or more copies of an isolated DNA [sequences as defined in any of claims 1 to 18] sequence encoding a polypeptide or

fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, and one or more copies of the DNA [sequences as defined in any of claims 19-26] sequence comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 7B, an amino acid sequence having at least 55% homology with the amino acid sequence of a 326 aa fragment from the C terminal end of the coding sequence of SEQ ID NO: 7B, SEQ ID NO: 8B, an amino acid sequence having at least 75% homology with the amino acid sequence of a 278 aa fragment from the C terminal end of the coding sequence of SEQ ID NO: 8B, SEQ ID NO: 9B, an amino acid sequence having at least 65% homology with the amino acid sequence of a 284 aa fragment from the C terminal end of the coding sequence of SEQ ID NO: 9B, SEQ ID NO: 10B, an amino acid sequence having at least 80% homology with the amino acid sequence of a 188 aa fragment from the C terminal end of the coding sequence of SEQ ID NO: 10B, SEQ ID NO: 11B, an amino acid sequence having at least 75% homology with the amino acid sequence of a 181 aa fragment from the 3' end of SEQ ID NO: 11B, SEQ ID NO: 12B, SEQ ID NO: 13B, an amino acid sequence having at least 55% homology with a 176 aa fragment from the C terminal end of the coding sequence of SEQ ID NO: 12B, and an amino acid sequence having at least 35% homology with a 284 aa fragment from the C terminal end of the coding sequence of SEQ ID NO: 13B, and a fragment of any thereof, said polypeptide or fragment thereof having alcohol dehydrogenase activity and being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit; and

feeding aldehydes and acyl-CoA to the microorganism, plant cell or plant.

39. (Amended) A method for producing aromatic and/or aliphatic esters in a microorganism, plant cell or plant, comprising:

inserting into the genome of the microorganism or plant one or more copies of an isolated DNA [sequences as defined in any of claims 1 to 18] sequence encoding a polypeptide or fragment

thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester

production in fruit, said polypeptide comprising an amino acid sequence selected from

the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO:

4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30%

homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology

with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ

ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B,

an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid

sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any

thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway

for aliphatic and/or aromatic ester production in fruit, and one or more copies of an

isolated DNA [sequences as defined in any of claims 19-26] sequence comprising an

amino acid sequence selected from the group consisting of: SEQ ID NO: 7B, an amino

acid sequence having at least 55% homology with the amino acid sequence of a 326 aa

fragment from the C terminal end of the coding sequence of SEQ ID NO: 7B, SEQ ID

NO: 8B, an amino acid sequence having at least 75% homology with the amino acid se-

quence of a 278 aa fragment from the C terminal end of the coding sequence of SEQ ID

NO: 8B, SEQ ID NO: 9B, an amino acid sequence having at least 65% homology with

the amino acid sequence of a 284 aa fragment from the C terminal end of the coding

sequence of SEQ ID NO: 9B, SEQ ID NO: 10B, an amino acid sequence having at least

80% homology with the amino acid sequence of a 188 aa fragment from the C terminal

end of the coding sequence of SEQ ID NO: 10B, SEQ ID NO: 11B, an amino acid

sequence having at least 75% homology with the amino acid sequence of a 181 aa

fragment from the 3' end of SEQ ID NO: 11B, SEQ ID NO: 12B, SEQ ID NO: 13B, an

amino acid sequence having at least 55% homology with a 176 aa fragment from the C terminal end of the coding sequence of SEQ ID NO:12B, and an amino acid sequence having at least 35% homology with a 284 aa fragment from the C terminal end of the coding sequence of SEQ ID NO: 13B, and a fragment of any thereof, said polypeptide or fragment thereof having alcohol dehydrogenase activity and being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit; and feeding alpha-keto acids and acyl-CoA to the microorganism, plant cell or plant.

Please cancel claims 41 and 42 without prejudice or disclaimer.

43. (Amended) A diagnostic kit for screening fruit with specific reference to volatile aliphatic and/or aromatic ester compounds comprising:

- a) one or more purified and isolated polypeptides, or fragments thereof, [as claimed is any of claims 19-26] involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said purified and isolated polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit; or
- b) one or more isolated DNA sequences [as claimed in any of claims 1-18,] encoding a polypeptide or fragment thereof, involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit, said polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1B, SEQ ID NO: 2B, SEQ ID NO: 3B, SEQ ID NO: 4B, SEQ ID NO: 5B, SEQ ID NO: 6B, an amino acid sequence having

at least 30% homology with SEQ ID NO: 1B, amino acid sequence having at least 40% homology with SEQ ID NO: 2B, an amino acid sequence having at least 80% homology with SEQ ID NO: 3B, an amino acid sequence having at least 90% homology with SEQ ID NO: 4B, an amino acid sequence having at least 90% homology SEQ ID NO: 5B, an amino acid sequence having at least 75% homology with SEQ ID NO: 6B, and a fragment of any thereof, said polypeptide or fragment thereof, being involved in the biosynthetic pathway for aliphatic and/or aromatic ester production in fruit; or

c). one or more antibodies as defined in claim 47].

Please cancel claim 44 without prejudice or disclaimer.